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OM protein - protein search, using sw model

Run on: December 2, 2005, 05:57:31 ; Search time 165 Seconds
(without alignments)
22.791 Million cell updates/sec

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPGQFAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pgp:*

2: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pgp:*

3: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pgp:*

4: /cgn2_6/prodata/1/pubpaa/US10A_PUBCOMB.pgp:*

5: /cgn2_6/prodata/1/pubpaa/US10B_PUBCOMB.pgp:*

6: /cgn2_6/prodata/1/pubpaa/US11_PUBCOMB.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	4	US-10-603-566-61
2	51	100.0	9	5	US-10-893-485-61
3	51	100.0	10	4	US-10-603-566-62
4	51	100.0	10	5	US-10-893-485-62
5	51	100.0	11	4	US-10-603-566-85
6	51	100.0	11	5	US-10-893-485-85
7	51	100.0	12	4	US-10-603-566-63
8	51	100.0	12	5	US-10-893-485-63
9	51	100.0	13	4	US-10-603-566-64
10	51	100.0	13	5	US-10-893-485-64
11	51	100.0	15	4	US-10-603-566-84
12	51	100.0	15	5	US-10-893-485-84
13	51	100.0	17	4	US-10-603-566-83
14	51	100.0	17	5	US-10-893-485-83
15	51	100.0	18	3	US-09-905-253A-31
16	51	100.0	18	4	US-10-201-187-31
17	51	100.0	19	4	US-10-603-566-22
18	51	100.0	19	4	US-10-603-566-53
19	51	100.0	19	5	US-10-893-485-22
20	51	100.0	19	5	US-10-893-485-53
21	51	100.0	20	4	US-10-603-566-54
22	51	100.0	20	5	US-10-893-485-54
23	51	100.0	25	4	US-10-603-566-52
24	51	100.0	25	5	US-10-893-485-52
25	51	100.0	137	4	US-10-603-566-14
26	51	100.0	137	5	US-10-893-485-14
27	51	100.0	143	4	US-10-603-566-12

28	51	100.0	143	5	US-10-893-485-12
29	51	100.0	157	4	US-10-201-187-48
30	51	100.0	157	4	US-10-603-566-73
31	51	100.0	157	5	US-10-893-485-73
32	51	100.0	160	3	US-09-925-301-945
33	51	100.0	163	3	US-09-905-253A-8
34	51	100.0	163	4	US-10-201-187-8
35	51	100.0	163	4	US-10-603-566-8
36	51	100.0	163	5	US-10-603-566-17
37	51	100.0	163	5	US-10-965-898-66
38	51	100.0	163	5	US-10-893-485-8
39	51	100.0	163	5	US-10-756-149-4779
40	51	100.0	163	5	US-10-958-527-5
41	48	94.1	9	4	US-10-603-566-71
42	48	94.1	9	5	US-10-893-485-71
43	47	92.2	9	5	US-10-893-485-97
44	47	92.2	13	4	US-10-603-566-91
45	47	92.2	13	5	US-10-893-485-91

ALIGNMENTS

RESULT 1

US-10-603-566-61
; Sequence 61, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergarde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-61

Query Match 100.0%; Score 51; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQFAFS 9
Db 1 YFPGQFAFS 9

RESULT 2

US-10-893-485-61
; Sequence 61, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbergarde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485

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; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-61

Query Match      100.0%; Score 51; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YFPGQFAFS 9
      |||||
Db      1 YFPGQFAFS 9

RESULT 3
US-10-603-566-62
; Sequence 62, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-62

Query Match      100.0%; Score 51; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YFPGQFAFS 9
      |||||
Db      2 YFPGQFAFS 10

RESULT 4
US-10-893-485-62
; Sequence 62, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc

; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-62

Query Match      100.0%; Score 51; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YFPGQFAFS 9
      |||||
Db      2 YFPGQFAFS 10

RESULT 5
US-10-603-566-85
; Sequence 85, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 85
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-85

Query Match      100.0%; Score 51; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YFPGQFAFS 9
      |||||
Db      3 YFPGQFAFS 11

RESULT 6
US-10-893-485-85
; Sequence 85, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
```

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; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 85
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-85
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Query Match 100.0%; Score 51; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 YFPGQFAFS 9
Db 3 YFPGQFAFS 11
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RESULT 7

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US-10-603-566-63
; Sequence 63, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-63
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Query Match 100.0%; Score 51; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 YFPGQFAFS 9
Db 4 YFPGQFAFS 12
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RESULT 8

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US-10-893-485-63
; Sequence 63, Application US/10893485
; Publication No. US20050155090A1
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; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-63
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Query Match 100.0%; Score 51; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 YFPGQFAFS 9
Db 4 YFPGQFAFS 12
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RESULT 9

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US-10-603-566-64
; Sequence 64, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-64
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Query Match 100.0%; Score 51; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 YFPGQFAFS 9
Db 5 YFPGQFAFS 13
```

RESULT 10

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US-10-893-485-64
; Sequence 64, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-64

Query Match      100.0%; Score 51; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
Db 5 YFPGQFAFS 13

RESULT 11
US-10-603-566-84
; Sequence 84, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-84

Query Match      100.0%; Score 51; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
Db 7 YFPGQFAFS 15

US-10-893-485-84
; Sequence 84, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-84

Query Match      100.0%; Score 51; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
Db 7 YFPGQFAFS 15

RESULT 13
US-10-603-566-83
; Sequence 83, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-83

Query Match      100.0%; Score 51; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
Db 7 YFPGQFAFS 15

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QY 1 YPFGQFAFS 9
| | | | | | | |
DB 9 YPFGQFAFS 17

Db | | | | | | | |
4 YPFGQFAFS 12

Search completed: December 2, 2005, 06:11:11
Job time : 166 secs

RESULT 14
US-10-893-485-83
; Sequence 83, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenberghe, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-83

Query Match 100.0%; Score 51; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPFGQFAFS 9
| | | | | | | |
DB 9 YPFGQFAFS 17

RESULT 15
US-09-905-253A-31
; Sequence 31, Application US/09905253A
; Publication No. US20030096299A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenberghe, Ann
; APPLICANT: Dethoux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Natural Ligand of G Protein Coupled Receptor ChemR23 and Uses Thereof
; FILE REFERENCE: 9409/2041
; CURRENT APPLICATION NUMBER: US/09/905,253A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-253A-31

Query Match 100.0%; Score 51; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPFGQFAFS 9

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 2, 2005, 05:49:41 ; Search time 47 Seconds
(without alignments)
15.832 Million cell updates/sec

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPGQFAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/prodata/1/iaa/5 COMB.pcp.*

2: /cgn2_6/prodata/1/iaa/6 COMB.pcp.*

3: /cgn2_6/prodata/1/iaa/7 COMB.pcp.*

4: /cgn2_6/prodata/1/iaa/PCITUS COMB.pcp.*

5: /cgn2_6/prodata/1/iaa/RE COMB.pcp.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	163	2	US-09-949-016-6284
2	51	100.0	166	2	US-09-949-016-11175
3	37	72.5	363	2	US-09-270-767-44161
4	37	72.5	422	2	US-09-949-016-8167
5	37	72.5	483	2	US-09-248-796A-20218
6	37	72.5	509	1	US-08-890-980-2
7	37	72.5	509	2	US-08-890-979-2
8	37	72.5	509	2	US-09-032-894-2
9	37	72.5	509	2	US-09-031-626-2
10	37	72.5	509	2	US-09-054-272-59
11	36	70.6	909	2	US-09-538-092-1315
12	36	70.6	1326	2	US-09-489-039A-7584
13	36	70.6	1330	2	US-09-543-681A-8057
14	35	68.6	31	1	US-08-190-802A-164
15	35	68.6	31	2	US-08-477-346-164
16	35	68.6	31	2	US-08-473-089-164
17	35	68.6	31	2	US-08-487-072A-164
18	35	68.6	255	2	US-09-902-540-12488
19	35	68.6	341	1	US-08-190-802A-45
20	35	68.6	341	2	US-08-477-346-45
21	35	68.6	341	2	US-08-473-089-45
22	35	68.6	341	2	US-08-487-072A-45
23	34	66.7	256	2	US-09-248-796A-20626
24	34	66.7	1299	2	US-09-252-991A-31121
25	33	64.7	121	2	US-09-991-433-26
26	33	64.7	121	2	US-10-014-012-214
27	33	64.7	122	2	US-10-014-012-213

28	33	64.7	169	2	US-09-489-039A-8257	Sequence 8257, Ap
29	33	64.7	170	2	US-09-775-925-31	Sequence 31, Appl
30	33	64.7	264	2	US-08-856-841-14	Sequence 14, Appl
31	33	64.7	287	2	US-09-248-796A-20338	Sequence 20338, A
32	33	64.7	395	2	US-08-856-841-13	Sequence 13, Appl
33	33	64.7	398	2	US-08-856-841-21	Sequence 21, Appl
34	33	64.7	415	2	US-08-856-841-20	Sequence 20, Appl
35	33	64.7	440	2	US-09-684-855-101	Sequence 101, App
36	33	64.7	440	2	US-09-684-855-124	Sequence 124, App
37	33	64.7	440	2	US-09-684-855-146	Sequence 146, App
38	33	64.7	440	2	US-09-488-265B-1	Sequence 1, Appli
39	33	64.7	443	2	US-09-902-540-14507	Sequence 14507, A
40	33	64.7	466	2	US-08-868-435-2	Sequence 2, Appli
41	33	64.7	466	2	US-08-744-231-2	Sequence 2, Appli
42	33	64.7	466	2	US-09-636-499-7	Sequence 7, Appli
43	33	64.7	466	2	US-09-273-871A-12	Sequence 12, Appl
44	33	64.7	466	2	US-10-083-452-12	Sequence 12, Appl
45	33	64.7	466	2	US-09-635-504-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-949-016-6284
; Sequence 6284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6284
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6284

Query Match 100.0%; Score 51; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.051; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9

Db 149 YFPGQFAFS 157

RESULT 2

US-09-949-016-11175
; Sequence 11175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11175
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11175

Query Match 100.0%; Score 51; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQFAPS 9
| | | | |
DB 152 YFPGQFAPS 160

RESULT 3
US-09-270-767-44161
; Sequence 44161, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44161
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-44161

Query Match 72.5%; Score 37; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQF 6
| | | | |
DB 27 YFPGQF 32

RESULT 4
US-09-949-016-8167
; Sequence 8167, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8167
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8167

Query Match 72.5%; Score 37; DB 2; Length 422;
Best Local Similarity 75.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAP 8
| | | | |
DB 262 YFPGMPPF 269

RESULT 5
US-09-248-796A-20218
; Sequence 20218, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248.796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20218
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-20218

Query Match 72.5%; Score 37; DB 2; Length 483;
Best Local Similarity 66.7%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFPGQFAPS 9
| | | | |
DB 399 FPGQFSVS 407

RESULT 6
US-08-890-980-2
; Sequence 2, Application US/08890980
; Patent No. 5998141
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSES: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,980
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

; MOLECULE TYPE: protein
US-08-890-980-2
Query Match 72.5%; Score 37; DB 1; Length 509;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAF 8
DB 194 YFPGMFPF 201

RESULT 7
US-08-890-979-2
; Sequence 2, Application US/08890979
; Patent No. 6030778
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
; TITLE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/890,979
; FILING DATE: 10-JUL-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-005.02
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-890-979-2

Query Match 72.5%; Score 37; DB 2; Length 509;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAF 8
DB 194 YFPGMFPF 201

RESULT 8
US-09-032-894-2
; Sequence 2, Application US/09032894
; Patent No. 6130041
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: SR-BI NUCLEIC ACIDS AND USES THEREFOR
; FILE REFERENCE: MIA-005.03
; CURRENT APPLICATION NUMBER: US/09/032,894
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,980

; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-031-626-2
; Sequence 2, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-031-626-2

Query Match 72.5%; Score 37; DB 2; Length 509;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAF 8
DB 194 YFPGMFPF 201

RESULT 9
US-09-031-626-2
; Sequence 2, Application US/09031626
; Patent No. 6228581
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Ordovas, Jose M.
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS AND
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS
; FILE REFERENCE: MIA-005.04
; CURRENT APPLICATION NUMBER: US/09/031,626
; CURRENT FILING DATE: 1998-02-27
; EARLIER APPLICATION NUMBER: 08/890,979
; EARLIER FILING DATE: 1997-07-10
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Human
US-09-031-626-2

Query Match 72.5%; Score 37; DB 2; Length 509;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAF 8
DB 194 YFPGMFPF 201

RESULT 10
US-09-054-272-59
; Sequence 59, Application US/09054272
; Patent No. 6692909
; GENERAL INFORMATION:
; APPLICANT: Lander, Eric S.
; APPLICANT: Daley, George O.
; APPLICANT: Cargill, Michele
; APPLICANT: Ireland, James S.
; APPLICANT: Rozen, Steven G.
; TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
; TITLE OF INVENTION: IN VASCULAR PATHOLOGY GENES
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
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; SOFTWARE: FastSeq for Windows version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WH198-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-054-272-59

Query Match 72.5%; Score 37; DB 2; Length 509;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAP 8
|:|:|:|
Db 194 YFPGMFPP 201

RESULT 11
US-09-538-092-1315
; Sequence 1315, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)-(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
; US-09-538-092-1315

Query Match 70.6%; Score 36; DB 2; Length 909;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAPS 9
|:|:|:|
Db 523 YFTGVFAPS 531

RESULT 12
US-09-489-039A-7584

; Sequence 7584, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7584
; LENGTH: 1326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-7584

Query Match 70.6%; Score 36; DB 2; Length 1326;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFPGQFAP 8
|:|:|:|
Db 509 YFPGQYEF 516

RESULT 13
US-09-543-681A-8057
; Sequence 8057, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRA.
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8057
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-09-543-681A-8057

Query Match 70.6%; Score 36; DB 2; Length 1330;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFPGQFAP 8
|:|:|:|
Db 508 YFPGQYEF 515

RESULT 14
US-08-190-802A-164
; Sequence 164, Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron, Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60850
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GTP binding prt squid r1v, Fig. 28
US-08-190-802A-164

Query Match 68.6%; Score 35; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YPFGQFAFS 9
DB 11 YPFGFAFA 19

RESULT 15
US-08-477-346-164
Sequence 164, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763

INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GTP binding prt squid r1v, Fig. 28
US-08-477-346-164

Query Match 68.6%; Score 35; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YPFGQFAFS 9
DB 11 YPFGFAFA 19

Search completed: December 2, 2005, 05:58:30
Job time : 48 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rnp) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:
<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2005, 05:45:20 ; Search time 234 Seconds
(without alignments)
27.136 Million cell updates/sec

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPQFAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	163	1	TIG2 HUMAN
2	51	100.0	163	1	TIG2 PONPY
3	51	100.0	163	2	O7LE52 HUMAN
4	47	92.2	163	1	TIG2_CRIGR
5	47	92.2	163	2	Q5BK77 RAT
6	44	86.3	1316	2	Q7MR17 WOLSU
7	42	82.4	500	2	Q989D1 RHILLO
8	41	80.4	162	1	TIG2 MOUSE
9	37	72.5	186	2	O516H6 ENTHI
10	37	72.5	227	2	Q6FPM5 ACIAD
11	37	72.5	258	2	Q7NAS9 MYCGA
12	37	72.5	267	2	Q8SVC7 ENCCU
13	37	72.5	276	2	Q7NV09 CHRVO
14	37	72.5	338	2	Q9SUG3 ARATH
15	37	72.5	341	2	Q7QCL7 ANOGA
16	37	72.5	342	2	Q8SYE1 DRONE
17	37	72.5	342	2	Q9W0U5 DRONE
18	37	72.5	509	2	Q521Z5 HUMAN
19	37	72.5	552	1	SCRBI HUMAN
20	37	72.5	564	2	Q5ATA8 CANAL
21	37	72.5	569	2	Q6BUU6 DEBHA
22	37	72.5	591	2	Q59FM4 HUMAN
23	37	72.5	636	2	Q87DL1 XYLFA
24	37	72.5	636	2	Q9PDC8 XYLFA
25	36	70.6	147	2	Q9QWK1 RAT
26	36	70.6	211	2	Q5XSV3 LEGPA
27	36	70.6	248	2	Q4ZM30 PSESY
28	36	70.6	248	2	Q88AH9 PSESM
29	36	70.6	342	2	Q4J8W1 SULAC
30	36	70.6	378	2	Q5L899 BACFN
31	36	70.6	378	2	Q64NJ9_BACFR

32	36	70.6	443	2	Q97WM0 SULSO
33	36	70.6	489	1	YM20_YEAST
34	36	70.6	586	2	Q8XPS3 RALSO
35	36	70.6	670	2	Q4QIY2 LEIMA
36	36	70.6	681	2	Q87AY1 XYLFT
37	36	70.6	842	2	Q8PN87_XANAC
38	36	70.6	858	2	O55157_RAT
39	36	70.6	858	2	Q4URW8_XANCP
40	36	70.6	861	2	Q8PBN1_XANCP
41	36	70.6	866	2	Q80XL8_MOUSE
42	36	70.6	909	1	CNGB1_HUMAN
43	36	70.6	938	2	O77658_BOVIN
44	36	70.6	948	2	O77659_BOVIN
45	36	70.6	949	2	Q8DMD5_SYNEL

Q97wm0	sulfolobus
P40210	saccharomyc
Q8xpe3	raistonia s
Q4qiy2	leishmania
Q87ay1	xylella fas
Q8pn87	xanthomonas
O55157	rattus norv
Q4urw8	xanthomonas
Q8pbn1	xanthomonas
Q80xl8	mus musculu
Q14028	homo sapien
O77658	bos taurus
O77659	bos taurus
Q8dmd5	synechococc

ALIGNMENTS

RESULT 1
TIG2_HUMAN STANDARD; PRT; 163 AA.
ID AC Q99969;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Retinoic acid receptor responder protein 2 precursor (Tazarotene-
DE induced gene 2 protein) (RAR-responsive protein TIG2).
DE Name=RARRES2; Synonyms=TIG2;
GN Homo sapiens (Human)
OS Homo sapiens
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NCBI_TaxID=9606;
RX MEDLINE=97348957; PubMed=9204961; DOI=10.1111/1523-1747.epi22276660;
RA Nagpal S., Patel S., Jacobs H., DiSepio D., Ghosh C., Malhotra M.,
RA Teng M., Duvic M., Chandraratna R.A.S.;
RT "Tazarotene-induced gene 2 (TIG2), a novel retinoid-responsive gene in
RT skin.";
RL J. Invest. Dermatol. 109:91-95(1997).
RN [1]
RP TISSUE=Skin;
RC TISSUE=Skin;
RX MEDLINE=97348957; PubMed=9204961; DOI=10.1111/1523-1747.epi22276660;
RA Nagpal S., Patel S., Jacobs H., DiSepio D., Ghosh C., Malhotra M.,
RA Teng M., Duvic M., Chandraratna R.A.S.;
RT "Tazarotene-induced gene 2 (TIG2), a novel retinoid-responsive gene in
RT skin.";
RL J. Invest. Dermatol. 109:91-95(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Gastric adenocarcinoma;
RX MEDLINE=99173880; PubMed=10072769; DOI=10.1016/S0378-1119(99)00004-9;
RA Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.;
RT "Selection of cDNAs encoding putative type II membrane proteins on the
RT cell surface from a human full-length cDNA bank.";
RL Gene 228:161-167(1999).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RX MEDLINE=12477932; PubMed=1247603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny K., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

```

RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -!- TISSUE SPECIFICITY: Highly expressed in skin (basal and suprabasal
CC layers of the epidermis, hair follicles and endothelial cells).
CC Also found in pancreas, liver, spleen, prostate, ovary, small
CC intestine and colon.
CC -!- INDUCTION: Inhibited in psoriatic lesions. Activated by tazarotene
CC in skin rafts and in the epidermis of psoriatic lesions.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U7594; AAB47975.1; -; mRNA.
DR EMBL; AB015632; BAA76499.1; -; mRNA.
DR EMBL; BC000069; AAH00069.1; -; mRNA.
DR Ensembl; ENSG00000106538; Homo sapiens.
DR HGNC; HGNC:9868; RARRES2.
DR H-InvDB; HIX0007202; -.
DR MIM; 601973; -.
DR GO; GO:0001523; P:retinoid metabolism; IDA.
DR Signal.
DR SIGNAL. 1 16 Potential.
FT CHAIN 17 163 Retinoic acid receptor responder protein
FT CHAIN 2.
FT SEQUENCE 163 AA; 18618 MW; A96EB7D0999EC3DB CRC64;
SQ
Query Match 100.0%; Score 51; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPFGQFAFS 9
Db 149 YPFGQFAFS 157

RESULT 2
TIG2_PONPY STANDARD; PRT; 163 AA.
AC QSR551;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Retinoic acid receptor responder protein 2 precursor.
DR Name=RARRES2;
GN Pongo pygmaeus (Orangutan).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1] NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Liver;
RC The German cDNA consortium;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CR861021; CAH93115.1; -; mRNA.
KW Signal.
FT SIGNAL. 1 20 Potential.
FT CHAIN 21 163 Retinoic acid receptor responder protein
FT CHAIN 2.
FT SEQUENCE 163 AA; 18644 MW; A96EB7D5D2D1726B CRC64;
SQ

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Query Match 100.0%; Score 51; DB 1; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPFGQFAFS 9
Db 149 YPFGQFAFS 157

RESULT 3
Q7LE02 HUMAN
ID O7LE02 HUMAN PRELIMINARY; PRT; 163 AA.
AC O7LE02;
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
DE Hypothetical protein RARRES2.
GN Name=RARRES2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1] NUCLEOTIDE SEQUENCE.
RP MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RX Haller L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Fowell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozerky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Rohlfing T., Rock S.M.,
RA Kozlowicz-Reilly A., Leonard S., Minx P., Maupin R., Strowatt C.,
RA Tin-Wollam A.-M., Abbott A., Johnson D., Murray J., Woessner J.P.,
RA Latreille P., Miller N., Johnson D., Minx P., Maupin R., Speith J.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flieck P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7."
RL Nature 424:157-164(2003).
RN [2] NUCLEOTIDE SEQUENCE.
RP Le T., Ozerky P., Stoneking T., Wohldmann P.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [3] NUCLEOTIDE SEQUENCE.
RP Waterston R.;
RA Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [4] NUCLEOTIDE SEQUENCE.
RP Waterston R.;
RA Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [5] NUCLEOTIDE SEQUENCE.
RP Wilson R.;
RA Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [6] NUCLEOTIDE SEQUENCE.
RP Halleck A., Ebert L., Mfoundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005586; AAS00384.1; -; genomic DNA.
DR EMBL; CR541992; CAG46789.1; -; mRNA.

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DR EMBL; CR542026; CAG46823.1; -, mRNA.
KW Hypothetical protein.
SQ SEQUENCE 163 AA; 18617 MW; A96EB7D0999EC3DB CRC64;

Query Match 100.08; Score 51; DB 2; Length 163;
Best Local Similarity 100.08; Pred. No. 0.091;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQPAFS 9
DB 149 YFPGQPAFS 157

RESULT 4
TIG2 CRIGR STANDARD; PRT; 163 AA.
AC Q8HDG8;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Retinoic acid receptor responder protein 2 precursor (Tazarotene-
DE induced gene 2 protein) (RAR-responsive protein TIG2).
GN Name=RARRES2; Synonyms=TIG2;
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Cricetidae; Cricetinae; Cricetulus.
OX NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=22499602; PubMed=12493756; DOI=10.1074/jbc.M210565200;
RA Satake H., Chen H.Y., Varki A.;
RT "Genes modulated by expression of GD3 synthase in Chinese hamster
RT ovary cells. Evidence that the Tis21 gene is involved in the induction
RT of GD3 9-O-acetylation.";
RJ J. Biol. Chem. 278:7942-7948(2003).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
KW EMBL; AB089674; BAC45229.1; -, mRNA.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 163 Retinoic acid receptor responder protein
FT FT 2.
SQ SEQUENCE 163 AA; 18707 MW; E705E0AA3447B3B8 CRC64;

Query Match 92.28; Score 47; DB 1; Length 163;
Best Local Similarity 88.94; Pred. No. 0.55;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQPAFS 9
DB 149 YFPGQPAFS 157

RESULT 5
Q5BK77 RAT PRELIMINARY; PRT; 163 AA.
AC Q5BK77;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Retinoic acid receptor responder (Tazarotene induced) 2
DE (predicted).
GN Name=Rarres2_predicted;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC091177; AAH91177.1; -, mRNA.
KW Receptor.
SQ SEQUENCE 163 AA; 18504 MW; A2D496F29F2D1BEE CRC64;

Query Match 92.28; Score 47; DB 2; Length 163;
Best Local Similarity 88.94; Pred. No. 0.55;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQPAFS 9
DB 149 YFPGQPAFS 157

RESULT 6
Q7MR17 WOLSU PRELIMINARY; PRT; 1316 AA.
AC Q7MR17;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=WS1797;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Kilmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes.";
RT Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR EMBL; BX571661; CAE10815.1; -, Genomic DNA.
DR GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
DR InterPro; IPR001434; DUF11.
DR TIGRfam; TIGR01451; B_ant_repeat; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1316 AA; 141999 MW; 48861B121C5E46E0 CRC64;
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Query Match 86.3%; Score 44; DB 2; Length 1316;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YPFGQFAPS 9
DB 579 YPFGULFAPS 587

RESULT 7

Q989D1 RHILLO PRELIMINARY; PRT; 500 AA.
AC Q989D1; RHILLO PRELIMINARY; PRT; 500 AA.
DT 01-OCT-2001 (TRENBLrel. 18, Created)
DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE M16478 protein.
GN OrderedLocustNames=m16478;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Ideawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL: BA000012; BAB52766.1; -; Genomic_DNA.
KW Complete proteome.
SQ SEQUENCE 500 AA; 5323 MW; 117D88E418223A5F CRC64;

Query Match 82.4%; Score 42; DB 2; Length 500;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YPFGQFAP 8
DB 236 YPFGNFAP 243

RESULT 8

TIG2 MOUSE STANDARD; PRT; 162 AA.
AC Q9DD06; Q8CHU8;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Retinoic acid receptor responder protein 2 precursor.
GN Name=Rarres2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=22354693; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragan T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

Grimmond S., Guetincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RL Nature 420:563-573(2002).
RN [2]

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT PHE-3.

STRAIN=FVB/N; TISSUE=Liver;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Small D.E.,
RA Schnerch A., Schein J.E., Jones J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.

EMBL: AK002298; BAB21997.1; -; mRNA.
DR EMBL: BC038914; AAH38914.1; -; mRNA.
DR Ensembl: ENSMUSG0000009281; Mus musculus.
DR MGI: MGI:1918910; Rarres2
DR GO: GO:0005615; C:extracellular space; TAS.
DR InterPro: IPR001894; Cathelicidin.
DR ProDom: PD001838; Cathelicidin; 1.
KW Polymorphism; Signal.

FT SIGNAL 1 19 Potential.
FT CHAIN 20 162 Retinoic acid receptor responder protein
FT VARIANT 3 C -> F (in strain FVB/N).
SQ SEQUENCE 162 AA; 18350 MW; 56FDE44B1BF167F3 CRC64;

Query Match 80.4%; Score 41; DB 1; Length 162;
Best Local Similarity 77.8%; Pred. No. 8.1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YPFGQFAPS 9
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Db 148 FLPQGFAPS 156

RESULT 9
Q516H6 ENTHI
ID Q516H6 ENTHI PRELIMINARY; PRT; 186 AA.
AC Q516H6;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Guanylate kinase, putative.
GN ORFNames=62.t000003;
OS Entamoeba histolytica HM-1:IMSS.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=294381;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HM-1:IMSS;
RX PubMed=15729342; DOI=10.1038/nature03291;
RA Loftus B., Anderson I., Davies R., Alsmark U.C., Samuelson J.,
RA Amedeo P., Roncaglia P., Berriman M., Hirt R.P., Mann B.J., Nozaki T.,
RA Suh B., Pop M., Duchene M., Ackers J., Tannich E., Leippe M.,
RA Hofer M., Bruchhaus I., Willhoft U., Bhattacharya A.,
RA Chillingworth T., Churcher C., Hance Z., Harris B., Harris D.,
RA Jagels K., Moule S., Mungall K., Ormond D., Squares R., Whitehead S.,
RA Quail M.A., Rabinowitz E., Norbertczak H., Price C., Wang Z.,
RA Guillen N., Gilchrist C., Stroup S.E., Bhattacharya S., Lohia A.,
RA Foster P.G., Sichert-Ponten T., Weber C., Singh U., Mukherjee C.,
RA El-Sayed N.M., Petri W.A., Clark C.G., Embley T.M., Barrell B.,
RA Fraser C.M., Hall N.;
RT "The genome of the protist parasite Entamoeba histolytica.";
RL Nature 433:865-868(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC ENBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
KW Kinase.
DR EMBL; AAF01000240; EAL48718.1; -; Genomic_DNA.
SQ SEQUENCE 186 AA; 21316 MW; C5AEF9CCAD6E6201 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 186;
Best Local Similarity 75.0%; Pred.No. 57;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FPGQGFAPS 9
|||:|
|||:|
Db 28 FPGKFSES 35

RESULT 10
Q6PFMS ACIAD
ID Q6PFMS ACIAD PRELIMINARY; PRT; 227 AA.
AC Q6PFMS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18).
GN OrderedLocusNames=ACIAD0159;
OS Acinetobacter sp. (strain ADP1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Moraxellaceae; Acinetobacter.
OX NCBI_TaxID=62977;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ADP1;
RX PubMed=15514110; DOI=10.1093/nar/gkh910;
RA Barbe V., Vallenet D., Fonknechten N., Kreimeyer A., Oztas S.,
RA Labarre L., Cruveiller S., Robert C., Duprat S., Wincker P.,
RA Ornstot L.N., Weissenbach J., Marliere P., Cohen G.N., Medigue C.;
RT "Unique features revealed by the genome sequence of Acinetobacter sp.
RT ADP1, a versatile and naturally transformation competent bacterium.";
RL Nucleic Acids Res. 32:5766-5779(2004).
DR EMBL; CR543861; CA667132.1; -; Genomic_DNA.
GO; GO:0004364; F:glutathione transferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR004045; GST_Cterm.
DR InterPro; IPR004045; GST_Nterm.
DR Pfam; PF00043; GST_C; 1.
DR Pfam; PF02798; GST_N; 1.
KW Complete proteome; Transferase.
SQ SEQUENCE 227 AA; 26580 MW; 4442PB5936F0C2EB CRC64;

Query Match 72.5%; Score 37; DB 2; Length 227;
Best Local Similarity 66.7%; Pred.No. 69;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
|||:|
|||:|
Db 175 YFAGQFSFA 183

RESULT 11
Q7NAS9 MYCGA
ID Q7NAS9 MYCGA PRELIMINARY; PRT; 258 AA.
AC Q7NAS9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Conserved hypothetical.
GN OrderedLocusNames=MYCGA5560; ORFNames=MGA_0316;
OS Mycoplasma gallisepticum.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2096;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=R;
RX MEDLINE=22830409; PubMed=12949158; DOI=10.1099/mic.0.26427-0;
RA Papaisi L., Gorton T.S., Kutish G., Markham P.F., Browning G.F.,
RA Nguyen D.K., Swartzell S., Madan A., Mahairas G., Geary S.J.;
RT "The complete genome sequence of the avian pathogen Mycoplasma
RT gallisepticum strain R(low).";
RL Microbiology 149:2307-2316(2003).
DR EMBL; AE016569; AAP56906.1; -; Genomic_DNA.
DR InterPro; IPR011631; DUF1600.
DR Pfam; PF07667; DUF1600; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 258 AA; 29973 MW; 058CC9102AC332F5 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 258;
Best Local Similarity 75.0%; Pred.No. 79;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFPGQFAF 8
|||:|
|||:|
Db 224 YFPGSFIF 231

RESULT 12
Q8SVC7 ENCCU
ID Q8SVC7 ENCCU PRELIMINARY; PRT; 267 AA.
AC Q8SVC7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein ECU06_0570.
GN OrderedLocusNames=ECU06_0570;
OS Eukaryota; Fungi; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806; DOI=10.1038/35106579;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thamarat F.,
RA Frensier G., Barbe V., Peyretallade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
```


RT "Genome sequence and gene compaction of the eukaryote parasite
 RL Encephalitozoon cuniculi.";

DR Nature 414:450-453(2001).
 DR EMBL; AL590446; CAD25417.1; -; Genomic DNA.
 DR GO; GO:0004519; F:endonuclease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR004042; Intein endonuc.
 DR PROSITE; PS50819; INTEIN_ENDONUCLEASE; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 267 AA; 30758 MW; D9E4B98F499AF639 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 267;

Best Local Similarity 75.0%; Pred. No. 82;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFPGQFAP 8

Db 165 FIPGQFAP 172

RESULT 13

Q7NY09 CHRVO

AC Q7NY09 CHRVO PRELIMINARY; PRT; 276 AA.

DT 01-MAR-2004 (TRENBLrel. 26, Created)

DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE Hypothetical protein.

GN OrderedLocusNames=CV1467;

OS Chromobacterium violaceum.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Chromobacterium.

OX NCBI_TaxID=536;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=ATCC 12472 / DSM 30191;

EX MEDLINE=2282880; PubMed=14500782; DOI=10.1073/pnas.1832124100;

RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,

RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,

RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Almeida M.F.,

RA Batista-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,

RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,

RA Bordignon J., Brigidio M.M., Brito C.A., Brocchi M., Burity H.A.,

RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,

RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,

RA Creczynski-Paga T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,

RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,

RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,

RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,

RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,

RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,

RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,

RA de Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,

RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,

RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,

RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Porrich D.P.,

RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,

RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunehz H.N.,

RA Silva A.M.R., da Silva A.L.C., Silva D.M., Silva R., Simoes I.C.,

RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,

RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,

RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;

RT "The complete genome sequence of Chromobacterium violaceum reveals

RT remarkable and exploitable bacterial adaptability.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).

DR EMBL; AE016915; RAQ59142.1; -; Genomic DNA.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 276 AA; 30415 MW; 2A0AC5C004F17573 CRC64;

Query Match 72.5%; Score 37; DB 2; Length 276;

Best Local Similarity 100.0%; Pred. No. 85;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQF 6

Db 149 YFPGQF 154

RESULT 14

Q9SUG3 ARATH

ID Q9SUG3 ARATH PRELIMINARY; PRT; 338 AA.

AC Q9SUG3 ARATH PRELIMINARY; PRT; 338 AA.

DT 01-MAY-2000 (TRENBLrel. 13, Created)

DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)

DT 01-FEB-2005 (TRENBLrel. 29, Last annotation update)

DE Inositol 1, 3, 4-trisphosphate 5/6-kinase-like protein.

GN Name=AT4G08170;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsals.

OX NCBI_TaxID=3702;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Bevan M., Lennard N., Quail M., Harris B., Rajandream M.A.,

RA Barrell B.G., Bancroft I., Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RA EU Arabidopsis sequencing project;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

RP NUCLEOTIDE SEQUENCE.

RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,

RA Mewes H.W., Lemcke K., Mayer K.F.X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

EMBL; AL080252; CAB45787.1; -; Genomic DNA.

DR EMBL; AL161510; CAB81153.1; -; Genomic DNA.

DR PIR; T10544;

DR GO; GO:0016301; F:kinase activity; IEA.

DR InterPro; IPR008656; Insl34_P3_kin.

DR Pfam; PF05770; Insl34_P3_kin; I.

KW Kinase.

SQ SEQUENCE 338 AA; 37987 MW; B1EC664D2B0DB2FA CRC64;

Query Match 72.5%; Score 37; DB 2; Length 338;

Best Local Similarity 75.0%; Pred. No. 1e+02;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFPGQFAP 8

Db 318 YFPGKDFD 325

RESULT 15

Q7QCL7 ANOGA

ID Q7QCL7 ANOGA PRELIMINARY; PRT; 341 AA.

AC Q7QCL7 ANOGA PRELIMINARY; PRT; 341 AA.

DT 01-MAR-2004 (TRENBLrel. 26, Created)

DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)

DE ENSANGP0000010778.

GN ORFNames=ENSANGG00000008289;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicidae;

OC Anophelinae; Anopheles.

OX NCBI_TaxID=180454;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;

RG The Anopheles gambiae Sequence Committee;

RT "Anopheles gambiae re-annotation.";

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PEST;
 RG The Anopheles gambiae Sequence Committee;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAB01008859; EAA08168.1; -; Genomic_DNA.
 DR InterPro; IPR011022; Arrestin_C.
 DR InterPro; IPR011021; Arrestin_N.
 DR Pfam; PF02752; Arrestin_C; 1.
 DR Pfam; PF00339; Arrestin_N; 1.
 SQ SEQUENCE 341 AA; 38842 MW; 8CBEDA6802AA74E CRC64;

Query Match 72.5%; Score 37; DB 2; Length 341;
 Best Local Similarity 100.0%; Pred.No. 1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YPFGQF 6
 |||||
 Db 19 YPFGQF 24

Search completed: December 2, 2005, 05:57:23
 Job time : 238 secs

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OM protein - protein search, using sw model

Run on: December 2, 2005, 05:31:45 ; Search time 187 Seconds
(without alignments)
21.147 Million cell updates/sec

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPGQFAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21.*

- 1: Geneseq1980s.*
- 2: Geneseq1990s.*
- 3: Geneseq2000s.*
- 4: Geneseq2001s.*
- 5: Geneseq2002s.*
- 6: Geneseq2003as.*
- 7: Geneseq2003bs.*
- 8: Geneseq2004s.*
- 9: Geneseq2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	100.0	9	9	Adw43837 Human che
2	51	100.0	9	9	Adw43915 ChemerinR
3	51	100.0	10	9	Adw43838 Human che
4	51	100.0	10	9	Adw43914 ChemerinR
5	51	100.0	11	9	Adw43861 Human che
6	51	100.0	11	9	Adw43913 ChemerinR
7	51	100.0	12	9	Adw43839 Human che
8	51	100.0	12	9	Adw43912 ChemerinR
9	51	100.0	13	9	Adw43911 ChemerinR
10	51	100.0	13	9	Adw43840 Human che
11	51	100.0	14	9	Adw43910 ChemerinR
12	51	100.0	15	9	Adw43909 ChemerinR
13	51	100.0	15	9	Adw43860 Human che
14	51	100.0	16	9	Adw43908 ChemerinR
15	51	100.0	17	9	Adw43907 ChemerinR
16	51	100.0	17	9	Adw43859 Human che
17	51	100.0	18	9	Adw43906 ChemerinR
18	51	100.0	18	9	Adx56680 Cardiovas
19	51	100.0	18	9	Ady38103 Human CPP
20	51	100.0	19	9	Adw43829 Human che
21	51	100.0	19	9	Adw43798 Human che
22	51	100.0	19	9	Adw43905 ChemerinR
23	51	100.0	20	9	Adw43830 Human che
24	51	100.0	20	9	Adw43904 ChemerinR

25	51	100.0	21	9	Adw43903	ChemerinR
26	51	100.0	22	9	Adw43902	ChemerinR
27	51	100.0	23	9	Adw43901	ChemerinR
28	51	100.0	24	9	Adw43900	ChemerinR
29	51	100.0	25	9	Adw43828	Human pro
30	51	100.0	25	9	Adw43899	ChemerinR
31	51	100.0	26	9	Adw43898	ChemerinR
32	51	100.0	27	9	Adw43897	ChemerinR
33	51	100.0	28	9	Adw43896	ChemerinR
34	51	100.0	29	9	Adw43895	ChemerinR
35	51	100.0	30	9	Adw43894	ChemerinR
36	51	100.0	31	9	Adw43893	ChemerinR
37	51	100.0	32	9	Adw43892	ChemerinR
38	51	100.0	33	9	Adw43891	ChemerinR
39	51	100.0	34	9	Adw43890	ChemerinR
40	51	100.0	35	9	Adw43889	ChemerinR
41	51	100.0	36	9	Adw43888	ChemerinR
42	51	100.0	37	9	Adw43887	ChemerinR
43	51	100.0	38	9	Adw43886	ChemerinR
44	51	100.0	39	9	Adw43885	ChemerinR
45	51	100.0	40	9	Adw43884	ChemerinR

ALIGNMENTS

RESULT 1

ADW43837

ID ADW43837 standard; peptide; 9 AA.

XX AC ADW43837;

XX AC ADW43837;

DT 24-MAR-2005 (first entry)

XX XX

DE Human chemerin peptide SEQ ID NO 61.

XX XX

KW gene therapy; diagnosis; cell signaling; gene therapy;

KW lymphoproliferative disease; dermatological disease; dermatological;

KW hemostatic; inflammation; antiinflammatory; hematological disease;

KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;

KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.

XX OS Homo sapiens.

XX PN WO200500875-A2.

XX XX

XX PD 06-JAN-2005.

XX XX

XX PF 25-JUN-2004; 2004WO-EP006945.

XX PR 25-JUN-2003; 2003US-00603566.

XX PA (EURO-) EUROSREEN SA.

XX PI Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;

XX PI Ooms FDR;

XX XX

XX DR WPI; 2005-058121/06.

XX XX

PT New Chemerin polypeptides, useful for diagnosing and treating a disease,

PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,

PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's

PT Disease, or histiocytosis.

XX Claim 5; SEQ ID NO 61; 183pp; English.

PS The invention describes a polypeptide (I) of up to 50 amino acids where

CC the polypeptide binds specifically to a chemerin polypeptide. Also

CC described are: a nucleic acid sequence encoding (I); an expression vector

CC comprising the coding sequence of the nucleic acid; a transgenic animal

CC transfected with the expression vector; a (therapeutic) composition

CC comprising (I) and an isolated chemerin polypeptide or a nucleic acid

CC sequence of (I); an antibody that selectively binds to (I); identifying

an agent that modulates the interaction between a Chemerin polypeptide and a Chemerin polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerin polypeptide and a Chemerin polypeptide in a sample; identifying an agent that modulates the function of Chemerin polypeptide; detecting the presence, in a sample, of an agent that modulates the function of Chemerin polypeptide; diagnosing a disease or disorder characterized by dysregulation of Chemerin (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of Chemerin polypeptide or for diagnosing a disease or disorder characterized by dysregulation of Chemerin polypeptide signaling, comprising an isolated Chemerin polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a Chemerin polynucleotide encoding (I); identifying an antibody inhibiting Chemerin activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human prochemerin peptide used to analyse processing of immature chemerin.

Sequence 9 AA;

Query Match 100.0%; Score 51; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YFGQGFAPS 9

Db 1 YFGQGFAPS 9

RESULT 2

ADW43915

ID ADW43915 standard; peptide; 9 AA.

XX AC ADW43915;

XX DT 24-MAR-2005 (first entry)

XX DE ChemerinR activation associated polypeptide #42.

XX KW gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic;
KW ChemerinR.

XX OS Unidentified.

XX PN WO200500875-A2.

XX PD 06-JAN-2005.

XX PF 25-JUN-2004; 2004WO-EP006945.

XX PR 25-JUN-2003; 2003US-00603566.

XX PA (EURO-) EUROSREEN SA.

XX PI Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;

XX PI Ooms FDR;

XX DR WPI; 2005-058121/06.

XX

PT New Chemerin polypeptides, useful for diagnosing and treating a disease,
PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,
PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
PT Disease, or histiocytosis.

XX PS Disclosure; Page 105; 183pp; English.

XX CC The invention describes a polypeptide (I) of up to 50 amino acids where
CC the polypeptide binds specifically to a ChemerinR polypeptide. Also
CC described are: a nucleic acid sequence encoding (I); an expression vector
CC comprising the coding sequence of the nucleic acid; a transgenic animal
CC transformed with the expression vector; a (therapeutic) composition
CC comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
CC sequence of (I); an antibody that selectively binds to (I); identifying
CC an agent that modulates the interaction between a Chemerin polypeptide
CC and a ChemerinR polypeptide; detecting the presence, in a sample, of an
CC agent that modulates the interaction between a Chemerin polypeptide and a
CC ChemerinR polypeptide in a sample; identifying an agent that modulates
CC the function of ChemerinR polypeptide; detecting the presence, in a
CC sample, of an agent that modulates the function of ChemerinR polypeptide;
CC diagnosing a disease or disorder characterized by dysregulation of
CC ChemerinR (polypeptide) signaling; a kit, for screening agents that
CC modulate the signaling activity of ChemerinR polypeptide or for
CC diagnosing a disease or disorder characterized by dysregulation of
CC ChemerinR polypeptide signaling, comprising an isolated ChemerinR
CC ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell
CC transformed with a polynucleotide encoding (I), and its packaging
CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
CC encoding (I); identifying an antibody inhibiting ChemerinR activation;
CC and an in vitro method of inhibiting cell proliferation. The
CC (therapeutic) composition or expression vector is useful for preparing a
CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
CC medicament for inhibiting cell proliferation, where the medicament is
CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
CC lymphoproliferative diseases, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
CC hyperproliferative disease. The polypeptides and polynucleotides and
CC methods are useful for diagnosing and treating the cited diseases. This
CC is the amino acid sequence of a polypeptide associated with activation of
CC the human chemerin receptor (chemerinR).

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 9; Length 9;

Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YFGQGFAPS 9

Db 1 YFGQGFAPS 9

RESULT 3

ADW43838

ID ADW43838 standard; peptide; 10 AA.

XX AC ADW43838;

XX XX 24-MAR-2005 (first entry)

XX DE Human chemerin peptide SEQ ID NO 62.

XX KW gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.

XX OS Homo sapiens.

XX XX WO2005000875-A2.

XX PN

CC sample, of an agent that modulates the function of Chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC ChemerinR (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of ChemerinR polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC ChemerinR polypeptide signaling, comprising an isolated ChemerinR
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting ChemerinR activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's
 CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a polypeptide associated with activation of
 CC the human chemerin receptor (chemerinR).
 XX

SEQ Sequence 11 AA;

Query Match 100.0%; Score 51; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.008;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
 |||||
 Db 3 YFPGQFAFS 11

RESULT 7

ADW43839
 ID ADW43839 standard; peptide; 12 AA.

XX AC ADW43839;

XX DT 24-MAR-2005 (first entry)

XX DE Human chemerin peptide SEQ ID NO 63.

XX gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
 OS Homo sapiens.

XX WO2005000875-A2.
 XX 06-JAN-2005.

XX 25-JUN-2004; 2004WO-EP006945.

XX 25-JUN-2003; 2003US-00603566.

XX (EURO-) EUROSCREEN SA.
 XX Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 PI Ooms FDR;

XX WPI; 2005-058121/06.

XX New Chemerin polypeptides, useful for diagnosing and treating a disease,
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
 PT sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's
 PT Disease, or histiocytosis.
 XX

PS Example 15; SEQ ID NO 63; 183pp; English.

XX The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a ChemerinR polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transformed with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a Chemerin polypeptide
 CC and a ChemerinR polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a Chemerin polypeptide and a
 CC ChemerinR polypeptide in a sample; identifying an agent that modulates
 CC the function of ChemerinR polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of ChemerinR polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC ChemerinR (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of ChemerinR polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC ChemerinR polypeptide signaling, comprising an isolated ChemerinR
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting ChemerinR activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's
 CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a human prochemerin peptide used to analyse
 CC processing of immature chemerin.
 XX

SEQ Sequence 12 AA;

Query Match 100.0%; Score 51; DB 9; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.0088;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9

|||||
 Db 4 YFPGQFAFS 12

RESULT 8

ADW43912
 ID ADW43912 standard; peptide; 12 AA.

XX AC ADW43912;

XX DT 24-MAR-2005 (first entry)

XX ChemerinR activation associated polypeptide #39.

XX gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.

XX Unidentified.

XX WO2005000875-A2.

XX 06-JAN-2005.

XX 25-JUN-2004; 2004WO-EP006945.

XX 25-JUN-2003; 2003US-00603566.

XX PA (EURO-) EUROSREEN SA.
 XX PI Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 XX PI Ooms FDR;
 XX PI WPI, 2005-058121/06.
 XX DR
 XX PT New Chemerin polypeptides, useful for diagnosing and treating a disease,
 XX PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
 XX PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
 XX PT Disease, or histiocytosis.
 XX PT
 XX PS Disclosure; Page 105; 183pp; English.
 XX CC
 CC The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a chemerin polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transfected with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated chemerin polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a chemerin polypeptide
 CC and a chemerin polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a chemerin polypeptide and a
 CC chemerin polypeptide in a sample; identifying an agent that modulates
 CC the function of chemerin polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC chemerin (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of chemerin polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC chemerin polypeptide signaling, comprising an isolated chemerin
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting chemerin activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
 CC Macroglobulinemia, Gaucher's disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a polypeptide associated with activation of
 CC the human chemerin receptor (chemerinR).
 XX SQ
 Query Match 100.0%; Score 51; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0088;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YPPGQFAPS 9
 DB 4 YPPGQFAPS 12
 RESULT 9
 ID ADW43911 standard; peptide; 13 AA.
 AC ADW43911;
 XX 24-MAR-2005 (first entry)
 DT
 XX ChemerinR activation associated polypeptide #38.
 DE
 XX gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW

KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.
 XX OS Unidentified.
 XX PN W02005000875-A2.
 XX PD 06-JAN-2005.
 XX PF 25-JUN-2004; 2004WO-EP006945.
 XX PR 25-JUN-2003; 2003US-00603566.
 XX PA (EURO-) EUROSREEN SA.
 XX PI Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 XX PI Ooms FDR;
 XX PI WPI, 2005-058121/06.
 XX DR
 XX PT New Chemerin polypeptides, useful for diagnosing and treating a disease,
 XX PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
 XX PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
 XX PT Disease, or histiocytosis.
 XX PT
 XX PS Disclosure; Page 105; 183pp; English.
 XX CC
 CC The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a chemerin polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transfected with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated chemerin polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a chemerin polypeptide
 CC and a chemerin polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a chemerin polypeptide and a
 CC chemerin polypeptide in a sample; identifying an agent that modulates
 CC the function of chemerin polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC chemerin (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of chemerin polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC chemerin polypeptide signaling, comprising an isolated chemerin
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting chemerin activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
 CC Macroglobulinemia, Gaucher's disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a polypeptide associated with activation of
 CC the human chemerin receptor (chemerinR).
 XX SQ
 Query Match 100.0%; Score 51; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0095;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YPPGQFAPS 9
 DB 5 YPPGQFAPS 13

CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a human prochemerin peptide used to analyse
 CC processing of immature chemerin.

XX SQ Sequence 13 AA;
 Query Match 100.0%; Score 51; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0095;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFFGQFAFS 9
 Db 5 YFFGQFAFS 13
 |||||

RESULT 11
 ADM43910
 ID ADM43910 standard; peptide; 14 AA.

XX AC ADM43910;
 XX DT 24-MAR-2005 (first entry)

XX ChemerinR activation associated polypeptide #37.

XX gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.

XX Unidentified.

XX WO2005000875-A2.

XX 06-JAN-2005.

XX 25-JUN-2004; 2004WO-BP006945.

XX 25-JUN-2003; 2003US-00603566.

(EURO-) EUROSREEN SA.

Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;

Ooms FDR;

WPI; 2005-058121/06.

New Chemerin polypeptides, useful for diagnosing and treating a disease,
 e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
 sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
 Disease, or histiocytosis.

Disclosure; Page 105; 183pp; English.

The invention describes a polypeptide (I) of up to 50 amino acids where
 the polypeptide binds specifically to a chemerinR polypeptide. Also
 described are: a nucleic acid sequence encoding (I); an expression vector
 comprising the coding sequence of the nucleic acid; a transgenic animal
 transfected with the expression vector; a (therapeutic) composition
 comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
 sequence of (I); an antibody that selectively binds to (I); identifying
 an agent that modulates the interaction between a Chemerin polypeptide
 and a ChemerinR polypeptide; detecting the presence, in a sample, of an
 agent that modulates the interaction between a Chemerin polypeptide and a
 ChemerinR polypeptide in a sample; identifying an agent that modulates
 the function of ChemerinR polypeptide; detecting the presence, in a
 sample, of an agent that modulates the function of ChemerinR polypeptide;
 diagnosing a disease or disorder characterized by dysregulation of
 ChemerinR (polypeptide) signaling; a kit, for screening agents that
 modulate the signaling activity of ChemerinR polypeptide or for
 diagnosing a disease or disorder characterized by dysregulation of

RESULT 10
 ADM43840
 ID ADM43840 standard; peptide; 13 AA.
 XX AC ADM43840;
 XX DT 24-MAR-2005 (first entry)
 XX Human chemerin peptide SEQ ID NO 64.

XX gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
 XX Homo sapiens.

XX WO2005000875-A2.

XX 06-JAN-2005.

XX 25-JUN-2004; 2004WO-EP006945.

XX 25-JUN-2003; 2003US-00603566.

XX (EURO-) EUROSREEN SA.

Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 Ooms FDR;

WPI; 2005-058121/06.

New Chemerin polypeptides, useful for diagnosing and treating a disease,
 e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
 sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
 Disease, or histiocytosis.

Example 15; SEQ ID NO 64; 183pp; English.

The invention describes a polypeptide (I) of up to 50 amino acids where
 the polypeptide binds specifically to a chemerinR polypeptide. Also
 described are: a nucleic acid sequence encoding (I); an expression vector
 comprising the coding sequence of the nucleic acid; a transgenic animal
 transfected with the expression vector; a (therapeutic) composition
 comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
 sequence of (I); an antibody that selectively binds to (I); identifying
 an agent that modulates the interaction between a Chemerin polypeptide
 and a ChemerinR polypeptide; detecting the presence, in a sample, of an
 agent that modulates the interaction between a Chemerin polypeptide and a
 ChemerinR polypeptide in a sample; identifying an agent that modulates
 the function of ChemerinR polypeptide; detecting the presence, in a
 sample, of an agent that modulates the function of ChemerinR polypeptide;
 diagnosing a disease or disorder characterized by dysregulation of
 ChemerinR (polypeptide) signaling; a kit, for screening agents that
 modulate the signaling activity of ChemerinR polypeptide or for
 diagnosing a disease or disorder characterized by dysregulation of
 ChemerinR polypeptide signaling, comprising an isolated ChemerinR
 polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 transfected with a polynucleotide encoding (I), and its packaging
 materials; a non-human mammal transgenic for a Chemerin polynucleotide
 encoding (I); identifying an antibody inhibiting ChemerinR activation;
 and an in vitro method of inhibiting cell proliferation. The
 (therapeutic) composition or expression vector is useful for preparing a
 medicament for ex vivo gene therapy or for in vivo gene therapy or a
 medicament for inhibiting cell proliferation, where the medicament is
 used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 lymphoproliferative diseases, disorders, and/or conditions,
 paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
 Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
 hyperproliferative disease. The polypeptides and polynucleotides and

XX WPI; 2005-058121/06.

XX New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's PT Disease, or histiocytosis.

XX Disclosure; SEQ ID NO 84; 183pp; English.

PS

XX The invention describes a polypeptide (I) of up to 50 amino acids where CC the polypeptide binds specifically to a chemerinR polypeptide. Also CC described are: a nucleic acid sequence encoding (I); an expression vector CC comprising the coding sequence of the nucleic acid; a transgenic animal CC transfected with the expression vector; a (therapeutic) composition CC comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid CC sequence of (I); an antibody that selectively binds to (I); identifying CC an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an CC agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; identifying an agent that modulates the presence, in a CC sample, of an agent that modulates the function of ChemerinR polypeptide; CC diagnosing a disease or disorder characterized by dysregulation of CC ChemerinR (polypeptide) signaling; a kit, for screening agents that CC modulate the signaling activity of ChemerinR polypeptide or for CC diagnosing a disease or disorder characterized by dysregulation of CC ChemerinR polypeptide signaling, comprising an isolated ChemerinR CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell CC transformed with a polynucleotide encoding (I), and its packaging CC materials; a non-human mammal transgenic for a Chemerin polynucleotide CC encoding (I); identifying an antibody inhibiting ChemerinR activation; CC and an in vitro method of inhibiting cell proliferation. The CC (therapeutic) composition or expression vector is useful for preparing a CC medicament for ex vivo gene therapy or for in vivo gene therapy or a CC medicament for inhibiting cell proliferation, where the medicament is CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, CC lymphoproliferative diseases, disorders, and/or conditions. CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other CC hyperproliferative disease. The polypeptides and polynucleotides and CC methods are useful for diagnosing and treating the cited diseases. This CC is the amino acid sequence of a human prochemerin peptide used to analyse CC processing of immature chemerin.

XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 51; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGQQAAPS 9
| | | | | | | | | |

Db 7 YFGQQAAPS 15

RESULT 14
ADW43908

ID ADW43908 standard; peptide; 16 AA.

XX

AC ADW43908;

XX

XX 24-MAR-2005 (first entry)

XX ChemerinR activation associated polypeptide #35.

DE

XX gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic;
KW chemerinR.

XX

OS Unidentified.

XX WO2005000875-A2.

XX 06-JAN-2005.

XX 25-JUN-2004; 2004WO-EP006945.

XX 25-JUN-2003; 2003US-00603566.

XX (EURO-) EUROSCREEN SA.

XX Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
PI Ooms FDR;

XX WPI; 2005-058121/06.

XX New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's PT Disease, or histiocytosis.

XX Disclosure; Page 104; 183pp; English.

XX The invention describes a polypeptide (I) of up to 50 amino acids where CC the polypeptide binds specifically to a chemerinR polypeptide. Also CC described are: a nucleic acid sequence encoding (I); an expression vector CC comprising the coding sequence of the nucleic acid; a transgenic animal CC transfected with the expression vector; a (therapeutic) composition CC comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid CC sequence of (I); an antibody that selectively binds to (I); identifying CC an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an CC agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; identifying an agent that modulates the presence, in a CC sample, of an agent that modulates the function of ChemerinR polypeptide; CC diagnosing a disease or disorder characterized by dysregulation of CC ChemerinR (polypeptide) signaling; a kit, for screening agents that CC modulate the signaling activity of ChemerinR polypeptide or for CC diagnosing a disease or disorder characterized by dysregulation of CC ChemerinR polypeptide signaling, comprising an isolated ChemerinR CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell CC transformed with a polynucleotide encoding (I), and its packaging CC materials; a non-human mammal transgenic for a Chemerin polynucleotide CC encoding (I); identifying an antibody inhibiting ChemerinR activation; CC and an in vitro method of inhibiting cell proliferation. The CC (therapeutic) composition or expression vector is useful for preparing a CC medicament for ex vivo gene therapy or for in vivo gene therapy or a CC medicament for inhibiting cell proliferation, where the medicament is CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, CC lymphoproliferative diseases, disorders, and/or conditions. CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other CC hyperproliferative disease. The polypeptides and polynucleotides and CC methods are useful for diagnosing and treating the cited diseases. This CC is the amino acid sequence of a polypeptide associated with activation of CC the human chemerin receptor (chemerinR).

XX

SQ Sequence 16 AA;

Query Match 100.0%; Score 51; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGQQAAPS 9
| | | | | | | | | |

Db 8 YFGQQAAPS 16

RESULT 15
ADW43907

ID ADW43907 standard; peptide; 17 AA.

XX ADW43907;
AC
XX
XX 24-MAR-2005 (first entry)
DE
XX ChemerinR activation associated polypeptide #34.
DE
XX gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antiinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen.; CNS-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic;
KW chemerinR.
XX
OS Unidentified.
XX
XX WO2005000875-A2.
PN
XX
PD 06-JAN-2005.
XX
XX 25-JUN-2004; 2004WO-EP006945.
PF
XX
XX 25-JUN-2003; 2003US-00603566.
PR
XX
XX (EURO-) EUROSREEN SA.
PA
XX
XX Wittamer V, Communi D, Dethoux M, Parmentier M, Loison C;
PI Ooms FDR;
PI
XX
DR WPI; 2005-058121/06.
XX
XX New Chemerin polypeptides, useful for diagnosing and treating a disease,
PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,
PT sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's
PT Disease, or histiocytosis.
XX
PS Disclosure; Page 104; 183pp; English.
XX
XX The invention describes a polypeptide (I) of up to 50 amino acids where
CC the polypeptide binds specifically to a chemerin polypeptide. Also
CC described are: a nucleic acid sequence encoding (I); an expression vector
CC comprising the coding sequence of the nucleic acid; a transgenic animal
CC transfected with the expression vector; a (therapeutic) composition
CC comprising (I) and an isolated chemerin polypeptide or a nucleic acid
CC sequence of (I); an antibody that selectively binds to (I); identifying
CC an agent that modulates the interaction between a chemerin polypeptide
CC and a chemerin polypeptide; detecting the presence, in a sample, of an
CC agent that modulates the interaction between a chemerin polypeptide and a
CC chemerin polypeptide in a sample; identifying an agent that modulates
CC the function of chemerin polypeptide; detecting the presence, in a
CC sample, of an agent that modulates the function of chemerin polypeptide;
CC diagnosing a disease or disorder characterized by dysregulation of
CC chemerin (polypeptide) signaling; a kit, for screening agents that
CC modulate the signaling activity of chemerin polypeptide or for
CC diagnosing a disease or disorder characterized by dysregulation of
CC chemerin polypeptide signaling, comprising an isolated chemerin
CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
CC transformed with a polynucleotide encoding (I), and its packaging
CC materials; a non-human mammal transgenic for a chemerin polynucleotide
CC encoding (I); identifying an antibody inhibiting chemerin activation;
CC and an in vitro method of inhibiting cell proliferation. The
CC (therapeutic) composition or expression vector is useful for preparing a
CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
CC medicament for inhibiting cell proliferation, where the medicament is
CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
CC lymphoproliferative diseases, disorders, and/or conditions,
CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's
CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
CC hyperproliferative disease. The polypeptides and polynucleotides and
CC methods are useful for diagnosing and treating the cited diseases. This
CC is the amino acid sequence of a polypeptide associated with activation of
CC the human chemerin receptor (chemerinR).
XX

SQ Sequence 17 AA;

Query Match 100.0%; Score 51; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQFAFS 9
|||
Db 9 YFPGQFAFS 17
|||

Search completed: December 2, 2005, 05:52:36
Job time : 188 secs

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November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases, older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **rnpbm** (Published Applications_NA_Main) and **rnpbm** (Published Applications_NA_New). Searches run against Amino Acid Published Applications produce two sets of results with the extensions **rapbm** (Published Applications_AA_Main) and **rapbm** (Published Applications_AA_New).

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OM protein - protein search, using sw model

Run on: December 2, 2005, 05:52:46 ; Search time 11 Seconds
(without alignments)
3.918 Million cell updates/sec

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPGQFAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_New:
1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	72.5	532	6 US-10-821-234-918	Sequence 918, App
2	32	62.7	116	7 US-11-174-186-18	Sequence 18, Appl
3	32	62.7	117	7 US-11-174-186-35	Sequence 35, Appl
4	32	62.7	259	6 US-10-512-184-31	Sequence 31, Appl
5	32	62.7	259	6 US-10-512-184-33	Sequence 33, Appl
6	32	62.7	329	6 US-10-512-184-68	Sequence 68, Appl
7	32	62.7	329	6 US-10-512-184-70	Sequence 70, Appl
8	32	62.7	397	6 US-10-467-657-4202	Sequence 4202, Ap
9	32	62.7	537	6 US-10-467-657-4136	Sequence 4136, Ap
10	32	62.7	579	7 US-11-174-186-41	Sequence 41, Appl
11	31	60.8	80	6 US-10-467-657-1620	Sequence 1620, Ap
12	31	60.8	301	6 US-10-131-826A-166	Sequence 166, Ap
13	30	58.8	372	6 US-10-793-626-1632	Sequence 1632, Ap
14	30	58.8	754	6 US-10-467-962B-63	Sequence 63, Appl
15	29	56.9	116	7 US-11-174-186-25	Sequence 25, Appl
16	29	56.9	117	6 US-10-467-657-9059	Sequence 9059, Ap
17	29	56.9	185	6 US-10-467-657-1228	Sequence 1228, Ap
18	29	56.9	564	7 US-11-082-389-78	Sequence 78, Appl
19	29	56.9	1627	6 US-10-821-234-1283	Sequence 1283, Ap
20	28	54.9	21	6 US-10-939-890-609	Sequence 609, App
21	28	54.9	60	7 US-11-091-668-8	Sequence 8, Appl
22	28	54.9	98	7 US-11-054-669-47	Sequence 47, Appl
23	28	54.9	98	7 US-11-084-554-58	Sequence 58, Appl
24	28	54.9	116	7 US-11-174-186-2	Sequence 2, Appl
25	28	54.9	116	7 US-11-174-186-26	Sequence 26, Appl

26	28	54.9	168	7 US-11-108-172-198	Sequence 198, App
27	28	54.9	199	7 US-11-113-424-44	Sequence 44, Appl
28	28	54.9	222	6 US-10-467-657-7108	Sequence 7108, Ap
29	28	54.9	253	7 US-11-054-515-1353	Sequence 1353, Ap
30	28	54.9	281	6 US-10-131-826A-372	Sequence 372, App
31	28	54.9	415	7 US-11-182-946-6	Sequence 6, Appl
32	28	54.9	435	6 US-10-467-657-4570	Sequence 4570, Ap
33	28	54.9	546	6 US-10-821-234-902	Sequence 902, App
34	28	54.9	742	6 US-10-558-986-2	Sequence 2, Appl
35	28	54.9	777	6 US-10-558-986-4	Sequence 4, Appl
36	27.5	53.9	735	7 US-11-184-380-24	Sequence 24, Appl
37	27	52.9	34	7 US-11-068-783-37	Sequence 37, Appl
38	27	52.9	56	6 US-10-467-657-948	Sequence 948, App
39	27	52.9	123	6 US-10-131-826A-402	Sequence 402, App
40	27	52.9	159	6 US-10-467-657-6388	Sequence 6388, Ap
41	27	52.9	192	6 US-10-467-657-5588	Sequence 5588, Ap
42	27	52.9	197	6 US-10-485-517-359	Sequence 359, App
43	27	52.9	228	6 US-10-848-689-1	Sequence 1, Appl
44	27	52.9	229	6 US-10-793-626-1986	Sequence 1986, Ap
45	27	52.9	251	6 US-10-512-184-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1

US-10-821-234-918
; Sequence 918, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 918
; LENGTH: 532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-918

Query Match 72.5%; Score 37; DB 6; Length 532;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAF 8

|||||
Db 217 YFPGMFPF 224

RESULT 2

US-11-174-186-18
; Sequence 18, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiang
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH7 heavy chain
US-11-174-186-18

Query Match 62.7%; Score 32; DB 7; Length 116;
Best Local Similarity .75.0%; Pred. No. 6.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAPS 9
| | | | |
Db 64 FKGRFAPS 71

RESULT 3

US-11-174-186-35
; Sequence 35, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 35
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH369 heavy chain
US-11-174-186-35

Query Match 62.7%; Score 32; DB 7; Length 117;
Best Local Similarity .75.0%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAPS 9
| | | | |
Db 64 FKGRFAPS 71

RESULT 4

US-10-512-184-31
; Sequence 31, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv VdCw with
; OTHER INFORMATION: specificity against Verticillium dahliae;
; OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match 62.7%; Score 32; DB 6; Length 259;
Best Local Similarity .75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAPS 9
| | | | |
Db 66 FKGRFAPS 73

RESULT 5

US-10-512-184-33
; Sequence 33, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
; OTHER INFORMATION: specificity against Phoma lingam; originates from
; OTHER INFORMATION: Mus musculus.
US-10-512-184-33

Query Match 62.7%; Score 32; DB 6; Length 259;
Best Local Similarity .75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAPS 9
| | | | |
Db 66 FKGRFAPS 73

RESULT 6

US-10-512-184-68
; Sequence 68, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur F"rderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match 62.7%; Score 32; DB 6; Length 329;
Best Local Similarity .75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAPS 9
| | | | |
Db 136 FKGRFAPS 143

RESULT 7
US-10-512-184-70
; Sequence 70, Application US/10512184
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant
; TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi
; FILE REFERENCE: 3581.01US01
; CURRENT APPLICATION NUMBER: US/10/512.184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 70
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: precursor
; OTHER INFORMATION: fusion protein comprising RS - linker - scfv VDM2.
US-10-512-184-70

Query Match 62.7%; Score 32; DB 6; Length 329;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAFS 9
|:|:|:|:
Db 136 FKGRFAFS 143

RESULT 8
US-10-467-657-4202
; Sequence 4202, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4202
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4202

Query Match 62.7%; Score 32; DB 6; Length 397;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 1 YPGQFAP 8
|:|:|:|:
Db 385 YPGKAAP 392

RESULT 9
US-10-467-657-4136
; Sequence 4136, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA

; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4136
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4136

Query Match 62.7%; Score 32; DB 6; Length 537;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YPGQFAFS 9
|:|:|:|:
Db 494 FPGQFGPA 502

RESULT 10
US-11-174-186-41
; Sequence 41, Application US/11174186
; Publication No. US2005024418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xing
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 41
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: heavy chain-IL2
US-11-174-186-41

Query Match 62.7%; Score 32; DB 7; Length 579;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAFS 9
|:|:|:|:
Db 64 FKGRFAFS 71

RESULT 11
US-10-467-657-1620
; Sequence 1620, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657


```
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 1620
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-1620

Query Match      60.8%; Score 31; DB 6; Length 80;
Best Local Similarity 71.4%; Pred. No. 7.1;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PQQFAFS 9
Db 63 PGRFAFN 69

RESULT 12
US-10-131-826A-166
; Sequence 166, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 166
; LENGTH: 301
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-131-826A-166
Query Match      60.8%; Score 31; DB 6; Length 301;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPGQ 5
Db 183 YFPGQ 187

RESULT 13
US-10-793-626-1632
; Sequence 1632, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1632
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1632

Query Match      58.8%; Score 30; DB 6; Length 372;
Best Local Similarity 71.4%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FPGQFAF 8
Db 329 YPGVFAF 335

RESULT 14
US-10-467-962B-63
; Sequence 63, Application US/10467962B
; Publication No. US20050246784A1
; GENERAL INFORMATION:
; APPLICANT: Plesch, Gunnar
; APPLICANT: Blau, Astrid
; APPLICANT: Daeschner, Klaus
; APPLICANT: Klein, Mathieu
; TITLE OF INVENTION: Identification of Herbicidally Active Substances
; FILE REFERENCE: 2000_857
; CURRENT APPLICATION NUMBER: US/10/467,962B
; CURRENT FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: PCT/EP02/01466
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn vers. 2.0
; SEQ ID NO 63
; LENGTH: 754
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-467-962B-63

Query Match      58.8%; Score 30; DB 6; Length 754;
Best Local Similarity 44.4%; Pred. No. 93;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPGQFAFS 9
Db 291 FPDQYTFN 299
```

RESULT 15
US-11-174-186-25
; Sequence 25, Application US/11174186
; Publication No. US20050244418A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Qian, Xiugi
; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
; FILE REFERENCE: LEX-019
; CURRENT APPLICATION NUMBER: US/11/174,186
; CURRENT FILING DATE: 2005-07-01
; PRIOR APPLICATION NUMBER: US 60/288,564
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: KS de-immunized VH5
US-11-174-186-25

Query Match 56.9%; Score 29; DB 7; Length 116;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 FPGQFAFS 9
Db 64 FKGRFAFT 71

Search completed: December 2, 2005, 05:58:47
Job time : 12 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 2, 2005, 05:45:05 ; Search time 37 Seconds
(without alignments)
23.404 Million cell updates/sec

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPQQAFAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	72.5	338	2 T10544	inositol 1,3,4-tri
2	37	72.5	509	1 A48528	membrane glycoprote
3	37	72.5	636	2 D82679	hypothetical prote
4	36	70.6	443	2 G90388	thermopsine precu
5	36	70.6	489	2 S50396	hypothetical prote
6	36	70.6	909	2 S32538	cGMP-gated cation
7	36	70.6	961	2 A82270	excinnuclease ABC c
8	36	70.6	970	2 S77349	excinnuclease ABC c
9	36	70.6	1310	1 I53597	proline dehydrogen
10	36	70.6	1320	1 D64843	proline dehydrogen
11	36	70.6	1320	1 S66279	proline dehydrogen
12	36	70.6	1320	2 A80633	proline dehydrogen
13	36	70.6	1320	2 D90786	proline dehydrogen
14	36	70.6	1320	2 B85646	proline dehydrogen
15	36	70.6	1323	2 AH0225	1-pyrroline-5-carb
16	35	68.6	341	1 RGO0BE	GTP-binding regula
17	35	68.6	1014	2 T36031	excinnuclease ABC c
18	34	66.7	248	2 S16417	homeotic protein H
19	34	66.7	281	2 A82104	conserved hypotchet
20	34	66.7	306	2 H75366	tRNA delta-2-isope
21	34	66.7	318	2 G70858	probable electron
22	34	66.7	318	2 T45397	FixB (imported) -
23	34	66.7	435	2 G86978	hypothetical prote
24	34	66.7	441	2 A70346	conserved hypotchet
25	34	66.7	499	2 T32888	hypothetical prote
26	34	66.7	662	2 H82401	conserved hypotchet
27	34	66.7	703	1 WMBET7	ULI17 protein - hum
28	33	64.7	141	2 B85865	hypothetical prote
29	33	64.7	141	2 C91021	hypothetical prote

30 33 64.7 141 2 AF0793 conserved hypotchet
31 33 64.7 141 2 A64996 Putative Nudix hyd
32 33 64.7 213 2 AH2636 conserved hypotchet
33 33 64.7 237 2 G97418 hypothetical prote
34 33 64.7 312 2 AB0302 hypothetical prote
35 33 64.7 387 2 A86302 hypothetical prote
36 33 64.7 408 2 AC1373 conserved hypotchet
37 33 64.7 545 2 T39499 conserved hypotchet
38 33 64.7 608 2 G75561 ABC transporter, A
39 33 64.7 681 2 E82612 outer membrane hem
40 33 64.7 740 2 D71602 hypothetical prote
41 33 64.7 781 1 VCPV19 coat protein VP1 -
42 33 64.7 940 1 BVCEUA excinnuclease ABC c
43 33 64.7 940 2 D86099 excinnuclease
44 33 64.7 940 2 H91258 excinnuclease
45 33 64.7 941 2 AE1017 excinnuclease

ALIGNMENTS

RESULT 1

T10544

inositol 1,3,4-trisphosphate 5/6-kinase homolog T12G13.10 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10544

R;Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Ban-
submitted to the Protein Sequence Database, June 1999

A;Reference number: Z16533

A;Accession: T10544

A;Molecule type: DNA

A;Residues: 1-338 <BEV>

A;Cross-references: UNIPROT:Q9SUG3; UNIPARC:UPI0000048910; EMBL:AL080252; GSPDB:GN000-

A;Experimental source: cultivar Columbia; BAC clone T12G13

C;Genetics:

A;Gene: ATSP:T12G13.10

A;Map position: 4

A;Introns: 65/2; 92/3; 103/3; 144/1; 175/1; 215/1; 274/1; 292/3

Query Match 72.5%; Score 37; DB 2; Length 338;

Best Local Similarity 75.0%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPQQAFA 8

Db 318 YFPQQAFA 325

RESULT 2

A48528

membrane glycoprotein CLA-1 protein long form precursor - human

N;Alternate names: CD36 and LIMP-II analogous-1 (CLA-1)

N;Contains: membrane glycoprotein CLA-1, short splice form

C;Species: Homo sapiens (man)

C;Date: 07-Apr-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C;Accession: S36656; A48528

R;Vega, M.

submitted to the EMBL Data Library, April 1993

A;Reference number: S36656

A;Accession: S36656

A;Molecule type: mRNA

A;Residues: 1-509 <VEG>

A;Cross-references: UNIPROT:Q8WTVO; UNIPARC:UPI0000073A04; EMBL:Z22555; NID:G397606; 1

A;Note: this sequence report represents the long form

R;Calvo, D.; Vega, M.A.

J. Biol. Chem. 268, 18929-18935, 1993

A;Title: Identification, primary structure, and distribution of CLA-1, a novel member

A;Reference number: A48528; MUID:93366811; PMID:7689561

A;Accession: A48528

A;Molecule type: mRNA

A;Residues: 1-42,143-509 <CAL>

A;Cross-references: UNIPARC:UPI0000174241; GB:Z22555

A>Note: this sequence report represents the short form; the long form was also sequenced

C:Genetics:

A:Gene: GDB:CD36L1

A:Cross-references: GDB:228074

A:Map position: 12pter-12qter

C:Superfamily: lysosomal integral membrane protein II

C:Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; myristyl

F:2-509/Product: membrane glycoprotein CLA-1, long splice form #status predicted <LMA>

F:2-42,143-509/Product: membrane glycoprotein CLA-1, short splice form #status predicted

F:2-8/Domain: intracellular #status predicted <Y1>

F:9-33/Domain: transmembrane #status predicted <Y1>

F:34-442/Domain: extracellular #status predicted <EXT>

F:443-464/Domain: transmembrane #status predicted <Y2>

F:465-509/Domain: intracellular #status predicted <Y2>

F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted

F:3/Binding site: palmitate (Cys) (covalent) #status predicted

F:102,108,173,212,227,255,310,330/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 72.5%; Score 37; DB 1; Length 509;

Best Local Similarity 75.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFPGQFAF 8
|||||

Db 194 YFPGMFPP 201

RESULT 3

D82679

hypothetical protein XP1451 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004

C:Accession: D82679

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A>Note: for a complete list of authors see reference number A59328 below

A:Accession: D82679

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-636 <SIM>

A:Cross-references: UNIPROT:Q9PDC8; UNIPARC:UPI00000C272B; GB:AE003849; NID

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Brienes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carrier, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matukuma, A.X.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsuchioka, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1451

Query Match 72.5%; Score 37; DB 2; Length 636;

Best Local Similarity 75.0%; Pred. No. 35;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFPGQFAF 8
|||||

Db 151 YFPGYFGP 158

RESULT 4

G90388

thermopsine precursor related protein [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C:Accession: G90388

R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Ch

Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder

arrett, R.A.; Ragan, M.A.; Seneen, C.W.; Van der Oost, J.

submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.

A:Reference number: A99139

A:Accession: G90388

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-443 <KUR>

A:Cross-references: UNIPROT:Q97WMO; UNIPARC:UPI0000064687; GB:AE006641; NID:G13815492

C:Genetics:

A:Gene: SSO2194

Query Match 70.6%; Score 36; DB 2; Length 443;

Best Local Similarity 66.7%; Pred. No. 38;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
|||||

Db 342 YFPGNFTLS 350

RESULT 5

S50396

hypothetical protein YMR140w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein YMR375.09

C:Species: Saccharomyces cerevisiae

C:Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004

C:Accession: S50396

R:Badcock, K.; Churcher, C.

submitted to the EMBL Data Library, December 1994

A:Reference number: S50388

A:Accession: S50396

A:Molecule type: DNA

A:Residues: 1-489 <BAD>

A:Cross-references: UNIPROT:P40210; UNIPARC:UPI00001388BA; EMBL:Z47071; NID:G606429;

C:Genetics:

A:Gene: MIPS:YMR140w

A:Cross-references: SGD:S0004748

A:Map position: 13R

Query Match 70.6%; Score 36; DB 2; Length 489;

Best Local Similarity 66.7%; Pred. No. 42;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
|||||

Db 277 YFPGPFNYS 285

RESULT 6

S32538

cGMP-gated cation channel 2, rod - human

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C:Accession: S32538

R:Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahamed, B.; Reed, R.R.; Yau, K.W.

Nature 362, 764-767, 1993

A:Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.

A:Reference number: S32538; MUID:93226050; PMID:7682292

A:Accession: S32538

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-909 <CHE>

A:Cross-references: UNIPROT:O43636; UNIPARC:UPI000017C0CA

C:Keywords: cGMP binding

F:620-742/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA

Query Match 70.6%; Score 36; DB 2; Length 909;

Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFPGQFAPS 9
| | | | | | | | | |
Db 523 YFTGVFAFS 531

RESULT 7
AE2270
excinuclease ABC chain A uvra [imported] - Nostoc sp. (strain PCC 7120)
N;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE2270
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AE2270
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-961 <KUR>
A;Cross-references: UNIPROT:Q8YQV0; UNIPARC:UPI00000CE8AA; GB:BA000019; PIDN:BAB75415.1;
C;Genetics:
A;Gene: uvra
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology

Query Match 70.6%; Score 36; DB 2; Length 961;
Best Local Similarity 66.7%; Pred. No. 82;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAPS 9
| | | | | | | | | |
Db 739 YKPGQFSFN 747

RESULT 8
S77349
excinuclease ABC chain A - Synecocystis sp. (strain PCC 6803)
N;Alternate names: protein slr1844; uvra protein
N;Contains: excision endonuclease ABC (EC 3.1.-.-) chain A
C;Species: Synecocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S77349
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-970 <KAN>
A;Cross-references: UNIPROT:P73412; UNIPARC:UPI0000137E9D; EMBL:D90906; GB:AB001339; NII
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
A;Gene: uvra
C;Function:
A;Description: has ATPase and DNA binding activity; involved in DNA repair
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology
C;Keywords: ATP; DNA binding; DNA repair; duplication; hydrolase; nucleotide binding; P-
F;34-41/Region: nucleotide-binding motif A (P-loop)
F;652-935/Domain: ATP-binding cassette homology <ABCE>
F;669-676/Region: nucleotide-binding motif A (P-loop)

Query Match 70.6%; Score 36; DB 2; Length 970;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAPS 9
| | | | | | | | | |
Db 754 YKPGQFSFN 762

RESULT 9
I53597
proline dehydrogenase (EC 1.5.99.8) / 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5
N;Contains: 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12); proline dehydrogen
C;Species: Escherichia coli
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: I53597; S43126
R;Xia, M.; Zhu, Y.; Cao, X.; You, L.; Chen, Z.
FEMS Microbiol. Lett. 127, 235-242, 1995
A;Title: Cloning, sequencing and analysis of a gene encoding Escherichia coli proline
A;Reference number: I53597; MUID:95278725; PMID:7758938
A;Accession: I53597
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1310 <XIA>
A;Cross-references: UNIPROT:Q59426; UNIPARC:UPI00000AB625; EMBL:X78340; NID:G467735;
A;Experimental source: strain K-12, substrain CSH4
C;Genetics:
A;Gene: putA
C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate deh
C;Keywords: PAD; flavoprotein; NAD; oxidoreductase
F;877/Active site: Glu #status predicted
F;911/Active site: Cys #status predicted

Query Match 70.6%; Score 36; DB 1; Length 1310;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAP 8
| | | | | | | | | |
Db 500 YPGQVEF 507

RESULT 10
D64843
proline dehydrogenase (EC 1.5.99.8) / 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5
N;Alternate names: proline oxidase
N;Contains: 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12); proline dehydrogen
C;Species: Escherichia coli
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: D64843; S53665; S53664; S07035
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: D64843
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1320 <BLAT>
A;Cross-references: UNIPROT:P09546; UNIPARC:UPI0000132B81; GB:AE000203; GB:U000096; NII
A;Experimental source: strain K-12, substrain MG1655
R;King, M.
submitted to the EMBL Data Library, January 1994
A;Reference number: S53665
A;Accession: S53665
A;Molecule type: DNA
A;Residues: 1-530, A', 532-1320 <LIN>
A;Cross-references: UNIPARC:UPI000016EC4A; EMBL:U05212; NID:G468874; PIDN:AAB59985.1;
A;Experimental source: strain K-12
R;King, M.; Allen, S.W.; Wood, J.M.
J. Mol. Biol. 243, 950-956, 1994
A;Title: Sequence analysis identifies the proline dehydrogenase and Delta(1)-pyrrolim
A;Reference number: S53664; MUID:95055736; PMID:7966312
A;Accession: S53664
A;Molecule type: DNA
A;Residues: 228-358; 404-446; 540-561; 651-1135 <LIW>

A;Cross-references: UNIPARC:UPI0000172085; UNIPARC:UPI0000172086; UNIPARC:UPI0000172087;
 R;Nakao, T.; Yamato, I.; Anraku, Y.
 Mol. Gen. Genet. 210, 364-369, 1987
 A;Title: Nucleotide sequence of putC, the regulatory region for the put regulon of Esche
 A;Reference number: S06385; MUID:88142554; PMID:3325781
 A;Accession: S07035
 A;Molecule type: DNA
 A;Residues: 1-19, 'F', 21-40, 'AR', 43-44, 'GKQRYGAGATCAAFWR' <NAK>
 A;Cross-references: UNIPARC:UPI0000172089; EMBL:X05653; NID:G42599; PIDN:CAA29141.1; PID
 C;Genetics:
 A;Gene: putA; poaA
 A;Map position: 23 min
 C;Function: <PDH>
 A;Description: EC 1.5.99.8 [validated, MUID:95055736]; transfers eletrons from proline b
 A;Pathway: proline utilization
 A;Note: membrane-bound with proline
 C;Function: <PCD>
 A;Description: EC 1.5.1.12 [validated, MUID:95055736]; catalyzes the hydrolysis of 1-pyr
 A;Pathway: proline utilization
 C;Function: <PREP>
 A;Description: controls the expression of the genes putP and putA in response to proline
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehyd
 C;Keywords: DNA binding; FAD; flavoprotein; membrane-associated protein; NAD; oxidoreduc
 F;883/Active site: Glu #status predicted
 F;911/Active site: Cys #status predicted

Query Match 70.6%; Score 36; DB 1; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAP 8
 Db 503 YYPGQYEF 510
 :|:|:|:|

RESULT 11
 S66279
 proline dehydrogenase (EC 1.5.99.8) / 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.
 C;Species: Salmonella typhimurium
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S66279; S33716; B39192; S03817; S31910
 R;Maloy, S.R.
 submitted to the EMBL Data Library, April 1994
 A;Reference number: S66279
 A;Accession: S66279
 A;Molecule type: DNA
 A;Residues: 1-1320 <MAL>
 A;Cross-references: UNIPROT:P10503; UNIPARC:UPI00001703CD; EMBL:X70843; NID:G470179; PID
 A;Experimental source: strain LT2
 A;Note: this is a revision to the sequence from reference S33716
 R;Allen, S.W.; Senti-Willis, A.; Maloy, S.R.
 Nucleic Acids Res. 21, 1676, 1993
 A;Title: DNA sequence of the putA gene from Salmonella typhimurium: a bifunctional membe
 A;Reference number: S33716; MUID:93241961; PMID:8479928
 A;Accession: S33716
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-19, 'WPRVSVIA', 28-272, 'ENWKR', 278-279, 'SAILTICWAN', 290-368, 'APKRRVWRSRSCW
 RSACVGRPASAIQRCRCRVNGYAWLMNRR', <ALL>
 A;Cross-references: UNIPARC:UPI0000172082; EMBL:X70843
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 A;Note: this sequence has been revised in reference S66279
 R;Ling, M.; Allen, S.W.; Wood, J.M.
 J. Mol. Biol. 243, 950-956, 1994
 A;Title: Sequence analysis identifies the proline dehydrogenase and Delta(1)-pyrroline-5
 A;Reference number: S53664; MUID:95055736; PMID:7966312
 A;Contents: annotation
 R;Ostrovsky de Spicer, P.; O'Brien, K.; Maloy, S.
 J. Bacteriol. 173, 211-219, 1991
 A;Title: Regulation of proline utilization in Salmonella typhimurium: a membrane-associat
 A;Reference number: A39192; MUID:91100285; PMID:1987118
 A;Accession: B39192
 A;Status: preliminary

A;Molecule type: DNA
 A;Residues: 1-26 <OST>
 A;Cross-references: UNIPARC:UPI0000172083
 A;Note: the authors translated the codon CGT for residue 24 as Gly
 R;Hahn, D.R.; Myers, R.S.; Kent, C.R.; Maloy, S.R.
 Mol. Gen. Genet. 213, 125-133, 1988
 A;Title: Regulation of proline utilization in Salmonella typhimurium: molecular chara
 A;Reference number: S03816; MUID:89127131; PMID:2851701
 A;Accession: S03817
 A;Molecule type: DNA
 A;Residues: 1-13, 'HARTDQ', 20-26 <HAH>
 A;Cross-references: UNIPARC:UPI0000172084; EMBL:X12569
 C;Genetics:
 A;Gene: putA
 A;Map position: 22 min
 C;Function:
 A;Description: transfers eletrons from proline to the respiratory chain; catalyzes pr
 A;Pathway: proline utilization
 A;Note: membrane-bound with proline
 C;Function: <HPC>
 A;Description: catalyzes hydrolysis of 1-pyrroline-5-carboxylate to gamma-glutamic ac
 A;Pathway: proline utilization
 C;Function: <RPA>
 A;Description: transcriptional repressor controls expression of genes putP and putA i
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate deh
 C;Keywords: DNA binding; FAD; flavoprotein; membrane-associated protein; NAD; oxidore
 F;883,917/Active site: Glu, Cys #status predicted

Query Match 70.6%; Score 36; DB 1; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAP 8
 Db 503 YYPGQYEF 510
 :|:|:|:|

RESULT 12
 AE0633
 proline dehydrogenase (proline oxidase) [imported] - Salmonella enterica subsp. enter
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 15-Mar-2004
 C;Accession: AE0633
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Ouail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A;Reference number: AE0502; MUID:21534947; PMID:11677608
 A;Accession: AE0633
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1320 <PAR>
 A;Cross-references: UNIPARC:UPI0000059FE0; GB:AL513382; PIDN:CAD08248.1; PID:gi650225
 C;Genetics:
 A;Gene: STY1159
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate del

Query Match 70.6%; Score 36; DB 2; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPGQFAP 8
 Db 503 YYPGQYEF 510
 :|:|:|:|

RESULT 13
 D90786
 proline dehydrogenase [imported] - Escherichia coli (strain O157:H7, substrain RIMD C
 C;Species: Escherichia coli

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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: D90786
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Sasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A;Reference number: A99629; PMID:21156231; PMID:11258796
A;Accession: D90786
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1320 <HAY>
A;Cross-references: UNIPROT:Q8XEG0; UNIPARC:UPI0000165406; GB:BA000007; PTDN:BA034683.1;
A;Experimental source: strain O157:H7, substrain RMD 0509952
C;Genetics:
A;Gene: ECel260
C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydr
Query Match 70.6%; Score 36; DB 2; Length 1320;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YPFGQFAP 8
DB 503 YPFGQYEF 510
RESULT 14
B85646
proline dehydrogenase, P5C dehydrogenase [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: B85646
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; PMID:21074935; PMID:11206551
A;Accession: B85646
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1320 <STO>
A;Cross-references: UNIPROT:Q8XEG0; UNIPARC:UPI000016575B; GB:AB005174; NID:gl2514374; E
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: putA
C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydr
Query Match 70.6%; Score 36; DB 2; Length 1320;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YPFGQFAP 8
DB 503 YPFGQYEF 510
RESULT 15
AH0225
1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) [imported] - Yersinia pestis (stra
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AH0225
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; PMID:21470413; PMID:11586360
A;Accession: AH0225
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1323 <KUR>
A;Cross-references: UNIPROT:Q8ZF67; UNIPARC:UPI00000CD862; GB:AL590842; PTDN:CAC90668.1;
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C;Genetics:
A;Gene: putA
C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate deh
C;Keywords: oxidoreductase
Query Match 70.6%; Score 36; DB 2; Length 1323;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 YPFGQFAP 8
DB 504 YPFGQYEF 511
Search completed: December 2, 2005, 05:53:21
Job time : 39 secs
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